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### **Crystal Structure Determination of Hex1**

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Beamline(s): X12C

**Introduction:** The Woronin body is a membrane bound organelle from filamentous fungi with function associated with the cellular response to cell lysis. Hex1 is localized to the matrix of the Woronin body from *N. crassa*. The expression of Hex1 in yeast generates hexagonal protein granules similar to the native Woronin body; suggestion a Hex1 encoded mechanism of Woronin body assembly. Hex1 deletion strain has no Woronin body and hyphae display a cytoplasmic bleeding phenotype in response to cells lysis<sup>1,2</sup>.

**Methods and Materials:** Hex1, 176 aa, is expressed as GST-fusion protein. Se-Met crystal (0.08 x 0.08 x 0.1 mm) and native crystal (0.2 x 0.2 x 0.2 mm) were grown from Hampton screen. Multiwavelength anomalous diffraction (MAD) data and native data were collected at beamline X12C at the NSLS. All collected data sets were processed with DENZO and reduced with the SCALEPACK. Five selenium positions were identified with program SOLVE. Phases were calculated and extended to 2.3 Å with PHASES package and further extended to 1.78 Å with native data when refined in CNS.

**Results:** The spacegroup of Hex1 is P6<sub>5</sub>22 with unitcell a = 57.427, c = 196.975 Å. The Se-Met crystal diffracts to 3 Å and the native crystal diffracts to 1.78 Å. The structure is currently at the final stages of refinement.

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### **References:**

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